REMARKS

Claims 34-37, 42-45, 66-69, 77, and 79-88 are pending in the application. Claims 1-33, 38-41, 46-65, 70-76, and 78 have been canceled without prejudice or disclaimer. New claims 79-88 have been added. Claims 34-37, 42-45, 66-69, and 77 are under active consideration.

Claims 37, 45, and 69 have been amended to further clarify that the nucleic acid sequence and a sequence having at least about 80% sequence identity thereto are recited in the claims. In addition, the claims have been amended to recite that the variant having 80% sequence identity is capable of expressing a fusion protein that elicits an immune response against HCV. Support for these amendments can be found in the specification, for example, at page 4, lines 3-12; page 9, lines 15-26; page 13, lines 27-29; page 15, lines 20-26; and page 19, lines 11-18. Accordingly, the specification provides adequate support for these amendments. Entry of the amendments is respectfully requested.

Claims 34, 42, and 66 have been amended to make explicit that the fusion protein is capable of eliciting an immunological response against HCV. Support for these amendments can be found in the specification, for example, at page 4, lines 3-12; page 13, lines 27-29; page 15, lines 6-7; and page 19, lines 11-18. Accordingly, the specification provides adequate support for these amendments. Entry of the amendments is respectfully requested.

Claims 1-33, 38-41, 46-65, 70-76, and 78 have been canceled without prejudice or disclaimer in order to remove non-elected subject matter. Applicants reserve the right to prosecute non-elected subject matter in subsequent divisional applications.

Support for new claims 79-88 can be found in the specification, for example, at page 4, lines 17-28; page 22, lines 16-26; page 26, lines 17-30; page 27, lines 21-30; page 28, lines 3-16. Entry of the new claims is respectfully requested.

Cancellation and amendment of the claims is made without prejudice, without intent to abandon any originally claimed subject matter, and without intent to acquiesce in any rejection of record. Applicants expressly reserve the right to file one or more continuing applications hereof containing the canceled or unamended claims.

Restriction Requirement

Applicants affirm the election without traverse of Group IV subgroup (B), which corresponds to claims 34-37, 42-45, 66-69, and 77, directed to nucleic acids encoding a fusion protein comprising an HBsAg S domain and an HCV E polypeptide, and the elected species of a chimeric HBsAg fused to an HCV E2 protein. Applicants submit that new claims 79 and 85-88 are drawn to substantially the same invention as the elected claims of Group IV, but are of a different scope. Therefore, Applicants respectfully request that new claims 79 and 85-88 be examined together with the elected claims of Group IV.

Rejoinder

Applicants request that new claims 80-82, drawn to methods of making the cell line of claim 77 (Group IV) and new claims 83 and 84 drawn to methods of using the cell line of claim 77, be rejoined per the Commissioner's Notice in the Official Gazette of March 26, 1996, entitled "Guidance on Treatment of Product and Process Claims in light of In re Ochiai, In re Brouwer and 35 U.S.C. § 103(b)" which sets forth the rules, upon allowance of product claims, for rejoinder of process claims covering the same scope of products. Applicants request that new claims 80-84 be rejoined and examined upon allowance of claim 77 drawn to the cell line of Group IV.

Objection to the Specification

The specification is objected to on the grounds that "it is unclear if, as the specification asserts on page 5, the E2 coding sequence begins at residue 1997; or if the E2 coding sequence actually begins at residue 2067, as is indicated by a comparison of the teachings on page 22 with the sequence disclosures in Choo and Figure 4" (Office Action, page 3).

The constuct pCMV-II-E2661-sAg (shown in Fig. 4A) and its nucleotide sequence (shown in Figs. 4B-4F and SEQ ID NO:6) includes the human tissue plasminogen activator (tpa) leader sequence at nucleotide positions 1992-2060 (encoding the 23 residue tpa signal peptide). The E2 coding sequence begins at nucleotide position

2067 and ends at nucleotide position 2900 of SEQ ID NO:6, and the sAg coding sequence begins at nucleotide position 2907 of SEQ ID NO:6. Applicants have amended the description of Figures 4A-4F at page 5 accordingly. Support for the amendment to the specification can be found in Figures 4A-4F, SEQ ID NO:6 of the Sequence Listing, and at page 26, line 20. No new matter is added by this amendment. Entry of the amendment to the specification and withdrawal of the objection to the specification is therefore respectfully requested.

Rejection under 35 U.S.C. § 101

Claims 34, 35, 37, 42, 45, 66, 67, and 69 have been rejected under 35 U.S.C. § 101 because the claimed invention is allegedly "not supported by either a specific and substantial utility or a well established utility" (Office Action, pages 4). In particular, the Office Action alleges:

> Because the ability of a polypeptide to induce an immune response against a specific pathogen is dependent on its sequence, and because there is no requirement in the claims that the variants of at least about 80% homology be able to induce an immune response against HCV, the application is claiming polypeptides for which there is no apparent utility. I.e., no utility has been asserted for immunogenic sequences of at least about 80% identity with the indicated E2 fragment which are not able to induce an immune response against HCV. The claims are therefore rejected as including embodiments for which no specific and substantial utility has been provided. (Office Action, page 4.)

Applicants respectfully submit that the current claims indeed comply with the utility requirement of 35 U.S.C. § 101. In particular, claims 34, 37, 42, 45, 66, and 69 have been amended to make explicit that the claimed nucleic acids encode fusion proteins capable of eliciting an immunological response against HCV. Such nucleic acids have utility in immunogenic compositions, such as HBV/HCV combination vaccines, for use in treating hepatitis infection. Immunogenic compositions comprising the claimed nucleic acids and methods of nucleic acid immunization are described in the specification, for example, at pages 29-37. Therefore, the claimed nucleic acids have a specific and substantial utility in treating hepatitis infection and meet the utility requirement under 35 U.S.C. § 101.

For at least these reasons, withdrawal of the rejection under 35 U.S.C. § 101 is respectfully requested.

Enablement Rejection under 35 U.S.C. § 112, first paragraph

Claims 34, 35, 37, 42, 45, 66, 67, and 69 have been rejected under 35 U.S.C. § 112, first paragraph on the grounds that "one skilled in the art clearly would not know how to use the claimed invention" because of the alleged lack of utility (Office Action, page 5). In particular, the Office Action alleges that "those in the art would not know how to use any protein with 80% identity to SEQ ID NO:6 absent such protein sharing at least one epitope with the included antigens" (Office Action, page 5). The Office Action further alleges that "those in the art have not been enabled for the making and use of any nucleic acid encoding any fusion protein of at least about 80% identity to residues to an HCV E2 protein, or to bases 1992-3584 of SEQ ID NO:6 (Office Action, page 5). Applicants respectfully traverse the rejection.

It is well settled that the test of enablement is whether one reasonably skilled in the art could make or use the invention from the disclosure in the patent coupled with information known in the art without undue experimentation. See, e.g., *Utter v. Hiraga*, 6 USPQ2d 1709, 1714 (Fed. Cir. 1988); *Hybritech, Inc. v. Monoclonal Antibodies, Inc.*, 231 USPQ 81, 94 (Fed. Cir. 1986); *Ex parte Forman*, 230 USPQ 546 (P.T.O. Bd. Pat. App. & Int., 1986). Specifically, in order to comply with the enablement requirement of 35 U.S.C. §112, first paragraph, the specification need only set forth such information as is sufficient to allow one of ordinary skill in the art to make and use the invention. How such a teaching is accomplished, either by the use of illustrative examples or by broad terminology, is of no importance since a specification which teaches how to make and use the invention in terms which correspond in scope to the claims must be taken as complying with the first paragraph of §112 unless there is reason to doubt the objective truth of the statements relied upon therein for enabling support (*In re Marzocchi*, 169 USPQ 367 (CCPA 1971)). The burden is on the Office to explain its reasons for the rejection and support the rejection with (i) acceptable evidence, or (ii) reasoning which contradicts the applicant's claim: the reasoning must be supported by current literature as

a whole and the Office must prove the disclosure requires undue experimentation. *In re Marzocchi*, 439 F.2d 220, 223-24, 169 USPQ 367, 369-70 (CCPA 1971). The Office has failed to carry its burden.

Applicants submit that more than adequate information has been provided in order to enable one of skill in the art to make and use the invention. In particular, the sequence for the reference nucleic acid encoding an E2 polypeptide (SEQ ID NO:6) is specified in the application in, *e.g.*, Figures 4A-4F. Given the information provided by SEQ ID NO:6, one of skill in the art would be able to routinely identify a nucleic acid comprising nucleotides 1992 through 3584 of SEQ ID NO:6, or the corresponding nucleotides from another HCV isolate, or a sequence having at least about 80% sequence identity to the sequence of SEQ ID NO:6. See the specification, for example, on page 15, line 29 through page 16, line 30, where it is noted how to determine sequences falling within the requisite percent identity. At the time of filing of the instant application, determining sequence identity was routine.

Furthermore, the specification also provides guidance on how to make the claimed nucleic acid variants encoding immunogenic HBV/HCV fusion proteins. Numerous sequences from different HCV strains that can be used in the practice of the invention are described in the specification, for example, at page 22, lines 2-15 and page 25, lines 1-16. Further, the identification of relevant polynucleotides encoding the variant polypeptides could be performed by hybridization and/or PCR techniques that were well-known to those skilled in the art at the time the subject application was filed (*e.g.*, page 17, lines 1-8). The specification also provides guidance on methods of making the HBV/HCV fusion constructs (e.g., pages 24-26). Moreover, the Examiner concedes that "many different HCV E2 polypeptide sequences were known in the art at the time the present application was filed. Additionally, the art indicates that the HCV E2 proteins contained epitopes within the regions of the E2 protein encoded by the claimed inventions" (Office Action, page 14).

Further, the specification describes methods of using the nucleic acids encoding HBV/HCV fusion proteins in immunogenic compositions such as vaccines (*e.g.*, pages 29-32) and methods of nucleic acid immunization for treatment of HCV infection (*e.g.*,

pages 32-37). The specification also provides guidance on methods of identifying nucleic acids that encode an immunogenic polypeptide capable of eliciting an immunological response against HCV. See the specification, for example, at Examples 1-5, which describe assays for detection of the expressed antigen (*e.g.*, page 38), detection of viral-like particles containing the expressed antigen (*e.g.*, pages 39-40, and measurement of antibody titers in response to nucleic acid immunization (*e.g.*, pages 41-42). Thus, the specification provides ample guidance as to methods of identification, generation, and use of the nucleic acids encoding immunogenic HBV/HCV fusion proteins of the claimed invention.

For at least the above reasons, withdrawal of the enablement rejection under 35 U.S.C. § 112 is respectfully requested.

Rejection under 35 U.S.C. § 112, second paragraph

Claims 37, 45, and 69 have been rejected under 35 U.S.C. § 112, second paragraph, as allegedly being "indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention." (Office Action, page 5). In particular, the Office Action alleges that "it is unclear whether the Applicant intended the term 'immunogenic' as a descriptor for the nucleic acid sequence itself, or the protein sequence encoded by the claimed nucleic acid" (Office Action, page 6).

Claims 37, 45, and 69 have been amended to make explicit that the nucleic acid sequence itself and a sequence having at least about 80% sequence identity thereto are recited in the claim. These amendments further clarify the intended subject matter of the claimed invention.

Therefore, Applicants respectfully request that the rejection under 35 U.S.C. § 112, second paragraph be withdrawn.

Rejection under 35 U.S.C. § 103

(1) Claims 34-36, 42-44, and 66-68 have been rejected under 35 U.S.C. § 103(a) as allegedly being unpatentable over the reference of Major et al. (J. Virol. 69:5798-5805) in view of the reference of Michalak et al. (J. Gen. Virol. 78:2299-2306) and

further in view of Valenzuela et al. (Bio/Technology 3:323-326). In particular, the Office Action alleges that it would have been obvious to use the E2 polypeptide disclosed by Michalak et al. in an immunogenic composition such as that disclosed by Major et al (Office Action, page 7). The Office Action further alleges that "the Valenzuela et al. reference also demonstrated success in the expression of a fusion protein comprising the S protein and a herpes virus antigen of about 300 amino acids – i.e. a fusion protein with a similar length to that of the fusion that would result from the combination of Michalak and Major. Those in the art would therefore have had a reasonable expectation of success in the expression of a similar-sized chimer comprising a HCV sequence rather than a herpesviral antigen." (Office Action, page 8.)

(2) In addition, claim 77 has been rejected under 35 U.S.C. § 103(a) as allegedly being unpatentable over the reference of Jacobs et al. (U.S. Patent No. 6,306,625) in view of Major et al., Michalak et al. and Valenzuela et al. as applied to claims 34-36, 42-44, and 66-68. In particular, the Office Action alleges that it would have been obvious to use HBsAg as a carrier molecule as described by Jacobs et al with the HCV antigenic sequences disclosed by Major et al., Michalak et al. and Valenzuela et al. and the cell lines described by Jacobs et al., comprising nucleic acids encoding such chimeric antigens in combination with nucleic acids encoding HBsAg, to produce virus-like particles comprising HBsAg and the chimeric antigens (Office Action, page 9).

(3) In addition, claim 37 has been rejected under 35 U.S.C. § 103(a) as allegedly being unpatentable over the reference of Jacobs et al. in view of Major et al., Michalak et al. and Valenzuela et al. as applied to claim 77, and further in view of GenBank Accesson Numbers X02763 and M62321. In particular, the Office Action alleges that the sequence of X02763, coding for HBsAg, is identical from bases 1564-2241 to the sequence of bases 2907-3583 of SEQ ID NO:6, and the sequence of M6231 coding for a portion of HCV E2, at bases 1491-2324 varies from the sequence of residues 2067-2900 of SEQ ID NO:6 by one amino acid (Office Action, page 10). The Office Action further alleges that it would have been obvious to combine the E2 and HBsAg sequences of GenBank Accession Numbers M62321 and X02763 as suggested by the teachings of Jacobs et al.

in view of Major et al., Michalak et al. and Valenzuela et al. to produce a nucleic acid with at least 80% identity to bases 1992-3584 of SEQ ID NO:6 (Office Action, page 11).

(4) In addition, claims 45 and 69 have been rejected under 35 U.S.C. § 103(a) as allegedly being unpatentable over the reference of Jacobs et al. in view of Major et al., Michalak et al. Valenzuela et al., and GenBank Accesson Numbers X02763 and M62321, as applied to claim 37, and further in view of the reference of Selby et al. (U.S. Patent No. 6,096,505) Chapman et al. (Nuc. Acids Res. 19:3979-3986), and Hartikka et al. (Hum. Gene Ther. 7:1205-1217). In particular, the Office Action alleges:

> From the combined teachings of Selby and Chapman, it would have been obvious to those in the art to use of [sic] pCMVII plasmid for the expression of the HBV/HCV chimer suggested by the previously cited references. This is because the art indicates that the inclusion of the CMV expression control sequences was beneficial to the protein expression. Although the pCMVII plasmid of Selby is different from that of pCMV6, the reference indicates that it was created to include the expression control sequences of pcMV6. Thus, those in the art would have had a reasonable expectation of success in the use of the pCMVII plasmid as a functional equivalent to the pCMV6 plasmid.
>
> Further, those in the art would also have had a reasonable expectation of success in the use of the plasmid in an immunogenic composition in view of the teachings of Hartikka. This is due to Hartikka's teachings regarding the use of plasmids with the same control sequences as the pCMVII vector for protein expression in mammals (see e.g., page 1209, Fig. 2), and suggestions for the use of such vectors in genetic vaccines (Page 1215).
>
> Thus, the Jacobs etc. references teach the described HBC/HCV chimer, and suggest the use of nucleic acids encoding such for genetic vaccination; whereas the teachings of Selby, Chapman, and Hartikka teach the pCMVII plasmid, and provide teachings indicating that the plasmid would be useful for protein expression in mammalian cells, and in genetic immunization. From these teachings, it would have been obvious to those in the art to use the pCMVII plasmid for the expression of the chimer suggested by Jacobs etc. because such a construction would result in a sequence varying from SEQ ID NO:6 by less than 80% (having only the differences identified with respect to claim 37 above), the combination of the cited references renders the claimed invention obvious. (Office Action, page 13.)

Applicants respectfully traverse the rejections under 35 U.S.C. § 103 on the following grounds.

To support an obviousness rejection under 35 U.S.C. § 103, "all the claim limitations must be taught or suggested by the prior art." M.P.E.P. § 2143.03. In addition, "the teaching or suggestion to make the claimed combination and the reasonable expectation of success must both be found in the prior art and not based on applicant's disclosure." M.P.E.P. § 706.02.

Applicants submit that the cited references do not disclose or suggest all the limitations of the present invention. Thus, a *prima facie* case of obviousness has not been presented by the Office, and the cited combination is based on impermissible hindsight reconstruction.

Major et al. fail to describe or suggest a nucleic acid encoding a fusion protein comprising HBsAg and an HCV E2 polypeptide, as claimed. Rather, Major et al. describe an HBsAg fusion with a polypeptide consisting of the first 58 residues of the HCV nucleocapsid, which includes a region of the core protein, but no part of the E2 protein of HCV. The text pointed out at page 5801 by the Examiner only shows results for an HBsAg fusion with an HCV core antigen, and contrary to the Examiner's assertions, does not show any results for a fusion containing an HCV E2 antigen. Nor does Major et al. suggest using an E2 antigen in place of the core antigen. Rather, Major et al. teach away from the use of the HCV envelope regions for immunization. Major et al. state that they performed immunization trials using the more conserved HCV capsid (core) antigen because of reports of the variability of the HCV envelope regions, which they believed bring into question the "suitability of these antigens in immunization programs" (see page 5804, col. 1). Thus, Major et al. fail to teach or suggest any type of fusion comprising HBsAg and an HCV E2 antigen.

The secondary references also fail to teach or suggest such fusions. Michalak et al. fail to describe or suggest any type of fusion comprising a combination of HBV and HCV antigens. Nor does Michalak et al. provide any motivation for using HBsAg to produce chimeric viral-like particles with HCV antigens. Valenzuela et al. also fail to describe or suggest any fusion of HBsAg with E2 antigens. Therefore, the references of Major et al., Michalak et al., and Valenzuela et al. do not teach or suggest all the limitations of claims 34-36, 42-44, and 66-68.

The reference of Jacobs et al. in view of the references of Major et al., Michalak et al., and Valenzuela et al. also fails to teach or suggest any fusions of HBsAG with HCV antigens. Nor does Jacobs et al. teach a cell line that expresses a virus-like particle comprising HBsAg and a chimeric antigen comprising a second HBsAg linked to an HCV immunogenic polypeptide. Therefore, no combination of the references of Jacobs et al., Major et al., Michalak et al., and Valenzuela et al. discloses or suggests all the limitations of claim 77.

As pointed out by the Examiner, the sequence disclosed in X02763 shares homology with SEQ ID NO:6 over only 676 residues from 2907 to 3583 of SEQ ID NO:6, that is, X02763 shares 42% identity with SEQ ID NO:6 over the 1592 residues of SEQ ID NO:6 from 1992 to 3584. The sequence disclosed in M62321 shares homology with SEQ ID NO:6 over only 833 residues from 1491 to 2324 of SEQ ID NO:6, that is, M62321 shares 52% identity with SEQ ID NO:6 over the 1592 residues of SEQ ID NO:6 from 1992 to 3584. Neither X02763 nor M62321 disclose a nucleotide sequence having at least about 80% sequence identity to a nucleic acid molecule comprising nucleotides 1992 through 3584 of SEQ ID NO:6, as required by claim 37 (see enclosed CLUSTALW alignments attached at Appendix A). Nor do X02763 and M62321 disclose the 75 nucleotides from 1992 to 2066 of SEQ ID NO:6 or the 6 nucleotides of SEQ ID NO:6 forming the "linker" between the end of the M62321 sequence and the beginning of the X02763 sequence. Applicants further note that the sequence of M62321 disclosed by Choo et al. encodes the entire HCV-1 polyprotein. Choo et al. fail to disclose or suggest what portion of the M62321 sequence encodes E2 in either their GenBank entry or their article (Proc. Natl. Acad. Sci. U.S.A. (1991) 88:2451-2455), nor make any mention of truncated forms of E2 or fusion proteins comprising HBsAg and E2. Moreover, no motivation can be found in either X02763 or M62321 or any of the other cited references for combining the two sequences as suggested by the Office Action. A reference cannot provide the motivation for combining an element that it never mentions or refers to. The showing that two references can be combined must be "clear and particular." See *In re Dembiczak* (CA FC) 50 USPQ2d 1614 (4/28/1999). Therefore, no combination of

the references of Jacobs et al., Major et al., Michalak et al., Valenzuela et al., and the sequences of X02763 and M62321 discloses or suggests all the limitations of claim 37.

Applicants note that the instant application, filed November 17, 2003, and the issued U.S. Patent No. 6,096,505 of Selby et al. share a common assignee, namely Chiron Corporation. Therefore, the reference of Selby et al. is disqualified as prior art under 35 U.S.C. § 103(c) since the subject matter of Selby et al. and the claimed invention were, at the time the inventions were made, owned by the same person or subject to an obligation of assignment to the same person. Thus, the rejection based on combination (4) above, relying on Selby et al., should be withdrawn.

Neither Chapman et al. nor Hartikka et al. disclose or suggest the pCMVII-E2661-sAg expression vector depicted in Figures 4A-4F and described in the specification, for example, at page 26, lines 17-29. The pCMV6 vector disclosed by Chapman et al. does not contain a bovine growth hormone polyA terminator (BGHt), or a coding sequence for a substantially complete S domain of HBsAg for expression of fusion proteins comprising HBsAg linked to an HCV immunogenic polypeptide. The vectors disclosed by Hartikka et al. lack the human tpa leader and the coding sequence for a substantially complete S domain of HBsAg, and in addition, are missing an *AmpR* ampicillin resistance gene. Furthermore, Chapman et al. and Hartikka et al. fail to describe or suggest any bicistronic construct or the inclusion of IRES sequences in vectors as recited in new claims 85-88. Neither Chapman et al. nor Hartikka et al. describe DNA immunization against hepatitis virus of any type.

None of the cited references predict the results observed from immunization with nucleic acids encoding a fusion protein comprising HBsAg and an HCV E2 polypeptide, as described in the specification. See, for example, Example 5, at pages 41-42, which describes the formation of chimeric HCV/HBV viral-like particles and anti-E2 antibody titers after DNA immunization.

The large number of references relied upon by the Examiner to show obviousness, as many as nine in number, in itself is evidence that the invention is not obvious. The invention must be considered as a whole, not reconstructed from bits and pieces of references based on hindsight. It is impermissible to apply an "obvious to try"

standard for a rejection under 35 U.S.C. § 103. As set forth by *In re Goodwin, Margrave, and Wagner*, 198 USPQ 1 (CCPA 1978):

> [T]his court has consistently refused to recognize "obvious to try" rejections. "As we have said many times, obvious to try is not the standard of 35 USC 103. In re Tomlinson, 53 CCPA 1421, 363 F.2d 928, 150 USPQ 623 (1966). Disregard for the unobviousness of the results of 'obvious to try' experiments disregards the 'invention as a whole' concept of §103 * * *." In re Antonie, 559 F.2d 618, 620, 195 USPQ 6, 8 (CCPA 1977) (emphasis in original).

Thus, the references do not disclose or suggest all the limitations of the present invention, and the Examiner has not met the burden of establishing a *prima facie* case of obviousness. In the absence of some teaching or suggestion in the cited references concerning nucleic acids encoding fusion proteins comprising HBsAg and an HCV E2 antigen, as described in the present application, the Examiner has presented no more than an improper hindsight reconstruction of the present invention. As stated by the Court of Appeals for the Federal Circuit *In re Fine*, 5 USPQ2d 1596, 1600 (Fed. Cir. 1988): "One cannot use hindsight reconstruction to pick and choose among isolated disclosures in the prior art to deprecate the claimed invention." Therefore, the Office has not met the requirements for a *prima facie* showing of obviousness under 35 U.S.C. § 103. For at least the above reasons, withdrawal of the rejections under 35 U.S.C. § 103(a) is respectfully requested.

CONCLUSION

In light of the above remarks, Applicant submits that the present application is fully in condition for allowance. Early notice to that effect is earnestly solicited.

If the Examiner contemplates other action, or if a telephone conference would expedite allowance of the claims, Applicants invite the Examiner to contact the undersigned.

The Commissioner is hereby authorized to charge any fees and credit any overpayment of fees which may be required under 37 C.F.R. §1.16, §1.17, or §1.21, to Deposit Account No. 18-1648.

Please direct all further written communications regarding this application to:

Michael J. Moran
Chiron Corporation
Intellectual Property - R440
P. O. Box 8097
Emeryville, CA 94662-8097
Tel: (510) 923-2969
Fax: (510) 655-3542

Respectfully submitted,

Date: October 31, 2005

By: Jenny Buchbinder

Jenny Buchbinder, Ph.D.
Registration No. 48,588
(650) 354-3383

CHIRON CORPORATION
Intellectual Property - R440
P. O. Box 8097
Emeryville, CA 94662-8097

Enclosures:
1. Appendix A: CLUSTALW alignments.

CLUSTALW Result

APPENDIX A

[clustalw.aln][clustalw.dnd][readme]

```
 CLUSTAL W (1.83) Multiple Sequence Alignments


Sequence type explicitly set to DNA
Sequence format is Pearson
Sequence 1: SEQIDNO_6_1992_3584     1593 bp
Sequence 2: M62321                  9401 bp
Start of Pairwise alignments
Aligning...


Sequences (1:2) Aligned. Score: 25.2982
Sequences (2:2) Aligned. Score: 39.7085
Guide tree        file created:   [clustalw.dnd]
Start of Multiple Alignment
There are 1 groups
Aligning...
Group 1:                    Delayed
Sequence:2     Score:22697
Alignment Score 7949
CLUSTAL-Alignment file created  [clustalw.aln]
```

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clustalw.aln

CLUSTAL W (1.83) multiple sequence alignment

```
SEQIDNO_6_1992_3584      ------------------------------------------------------------
M62321                   GCCAGCCCCCTGATGGGGGCGACACTCCACCATGAATCACTCCCCTGTGAGGAACTACTG

SEQIDNO_6_1992_3584      ------------------------------------------------------------
M62321                   TCTTCACGCAGAAAGCGTCTAGCCATGGCGTTAGTATGAGTGTCGTGCAGCCTCCAGGAC

SEQIDNO_6_1992_3584      ------------------------------------------------------------
M62321                   CCCCCCTCCCGGGAGAGCCATAGTGGTCTGCGGAACCGGTGAGTACACCGGAATTGCCAG

SEQIDNO_6_1992_3584      ------------------------------------------------------------
M62321                   GACGACCGGGTCCTTTCTTGGATCAACCCGCTCAATGCCTGGAGATTTGGGCGTGCCCCC

SEQIDNO_6_1992_3584      ------------------------------------------------------------
M62321                   GCAAGACTGCTAGCCGAGTAGTGTTGGGTCGCGAAAGGCCTTGTGGTACTGCCTGATAGG

SEQIDNO_6_1992_3584      ------------------------------------------------------------
M62321                   GTGCTTGCGAGTGCCCCGGGAGGTCTCGTAGACCGTGCACCATGAGCACGAATCCTAAAC

SEQIDNO_6_1992_3584      ------------------------------------------------------------
M62321                   CTCAAAAAAAAAACAAACGTAACACCAACCGTCGCCCACAGGACGTCAAGTTCCCGGGTG
```

```
SEQIDNO_6_1992_3584     ------------------------------------------------------------
M62321                  GCGGTCAGATCGTTGGTGGAGTTTACTTGTTGCCGCGCAGGGGCCCTAGATTGGGTGTGC

SEQIDNO_6_1992_3584     ------------------------------------------------------------
M62321                  GCGCGACGAGAAAGACTTCCGAGCGGTCGCAACCTCGAGGTAGACGTCAGCCTATCCCCA

SEQIDNO_6_1992_3584     ------------------------------------------------------------
M62321                  AGGCTCGTCGGCCCGAGGGCAGGACCTGGGCTCAGCCCGGGTACCCTTGGCCCCTCTATG

SEQIDNO_6_1992_3584     ------------------------------------------------------------
M62321                  GCAATGAGGGCTGCGGGTGGGCGGGATGGCTCCTGTCTCCCCGTGGCTCTCGGCCTAGCT

SEQIDNO_6_1992_3584     ------------------------------------------------------------
M62321                  GGGGCCCCACAGACCCCCGGCGTAGGTCGCGCAATTTGGGTAAGGTCATCGATACCCTTA

SEQIDNO_6_1992_3584     ------------------------------------------------------------
M62321                  CGTGCGGCTTCGCCGACCTCATGGGGTACATACCGCTCGTCGGCGCCCCTCTTGGAGGCG

SEQIDNO_6_1992_3584     ------------------------------------------------------------
M62321                  CTGCCAGGGCCCTGGCGCATGGCGTCCGGGTTCTGGAAGACGGCGTGAACTATGCAACAG

SEQIDNO_6_1992_3584     ------------------------------------------------------------
M62321                  GGAACCTTCCTGGTTGCTCTTTCTCTATCTTCCTTCTGGCCCTGCTCTCTTGCTTGACTG

SEQIDNO_6_1992_3584     ------------------------------------------------------------
M62321                  TGCCCGCTTCGGCCTACCAAGTGCGCAACTCCACGGGGCTTTACCACGTCACCAATGATT

SEQIDNO_6_1992_3584     ------------------------------------------------------------
M62321                  GCCCTAACTCGAGTATTGTGTACGAGGCGGCCGATGCCATCCTGCACACTCCGGGGTGCG

SEQIDNO_6_1992_3584     ------------------------------------------------------------
M62321                  TCCCTTGCGTTCGTGAGGGCAACGCCTCGAGGTGTTGGGTGGCGATGACCCCTACGGTGG

SEQIDNO_6_1992_3584     ------------------------------------------------------------
M62321                  CCACCAGGGATGGCAAACTCCCCGCGACGCAGCTTCGACGTCACATCGATCTGCTTGTCG

SEQIDNO_6_1992_3584     ------------------------------------------------------------
M62321                  GGAGCGCCACCCTCTGTTCGGCCCTCTACGTGGGGGACCTATGCGGGTCTGTCTTTCTTG

SEQIDNO_6_1992_3584     ------------------------------------------------------------
M62321                  TCGGCCAACTGTTCACCTTCTCTCCCAGGCGCCACTGGACGACGCAAGGTTGCAATTGCT

SEQIDNO_6_1992_3584     ------------------------------------------------------------
M62321                  CTATCTATCCCGGCCATATAACGGGTCACCGCATGGCATGGGATATGATGATGAACTGGT

SEQIDNO_6_1992_3584     ------------------------------------------------------------
M62321                  CCCCTACGACGGCGTTGGTAATGGCTCAGCTGCTCCGGATCCCACAAGCCATCTTGGACA
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```
SEQIDNO_6_1992_3584     --------------------ATGGATGCAATGAAGAGAGGGCTCTGCTGTGTGCTGCTGC
M62321                  TGATCGCTGGTGCTCACTGGGGAGTCCTGGCGGGCATAGCGTATTTCTCCATGGTGGGGA
                                            *       *   * ** *   * **   ** **  *

SEQIDNO_6_1992_3584     TGTGTGGAGCAGTCTTCGTTTCGC------------CCAGCGCTAGCG---AAACCCACG
M62321                  ACTGGGCGAAGGTCCTGGTAGTGCTGCTGCTATTTGCCGGCGTCGACGCGGAAACCCACG
                          ** *     *** * **   **            ** ***    **   *********

SEQIDNO_6_1992_3584     TCACCGGGGGAAGTGCCGGCCACACTGTGTCTGGATTTGTTAGCCTCCTCGCACCAGGCG
M62321                  TCACCGGGGGAAGTGCCGGCCACACTGTGTCTGGATTTGTTAGCCTCCTCGCACCAGGCG
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SEQIDNO_6_1992_3584     CCAAGCAGAACGTCCAGCTGATCAACACCAACGGCAGTTGGCACCTCAATAGCACGGCCC
M62321                  CCAAGCAGAACGTCCAGCTGATCAACACCAACGGCAGTTGGCACCTCAATAGCACGGCCC
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SEQIDNO_6_1992_3584     TGAACTGCAATGATAGCCTCAACACCGGCTGGTTGGCAGGGCTTTTCTATCACCACAAGT
M62321                  TGAACTGCAATGATAGCCTCAACACCGGCTGGTTGGCAGGGCTTTTCTATCACCACAAGT
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SEQIDNO_6_1992_3584     TCAACTCTTCAGGCTGTCCTGAGAGGCTAGCCAGCTGCCGACCCCTTACCGATTTTGACC
M62321                  TCAACTCTTCAGGCTGTCCTGAGAGGCTAGCCAGCTGCCGACCCCTTACCGATTTTGACC
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SEQIDNO_6_1992_3584     AGGGCTGGGGCCCTATCAGTTATGCCAACGGAAGCGGCCCCGACCAGCGCCCCTACTGCT
M62321                  AGGGCTGGGGCCCTATCAGTTATGCCAACGGAAGCGGCCCCGACCAGCGCCCCTACTGCT
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SEQIDNO_6_1992_3584     GGCACTACCCCCCAAAACCTTGCGGTATTGTGCCCGCGAAGAGTGTGTGTGGTCCGGTAT
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SEQIDNO_6_1992_3584     ATTGCTTCACTCCCAGCCCCGTGGTGGTGGGAACGACCGACAGGTCGGGCGCGCCCACCT
M62321                  ATTGCTTCACTCCCAGCCCCGTGGTGGTGGGAACGACCGACAGGTCGGGCGCGCCCACCT
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SEQIDNO_6_1992_3584     ACAGCTGGGGTGAAAATGATACGGACGTCTTCGTCCTTAACAATACCAGGCCACCGCTGG
M62321                  ACAGCTGGGGTGAAAATGATACGGACGTCTTCGTCCTTAACAATACCAGGCCACCGCTGG
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SEQIDNO_6_1992_3584     GCAATTGGTTCGGTTGTACCTGGATGAACTCAACTGGATTCACCAAAGTGTGCGGAGCGC
M62321                  GCAATTGGTTCGGTTGTACCTGGATGAACTCAACTGGATTCACCAAAGTGTGCGGAGCGC
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M62321                  GCCTGGTCGACTACCCGTATAGGCTTTGGCATTATCCTTGTACCATCAACTACACCATAT
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M62321                  TTAAAATCAGGATGTACGTGGGAGGGGTCGAACACAGGCTGGAAGCTGCCTGCAACTGGA
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SEQIDNO_6_1992_3584     ACATCACATCAGGATTCCTAGGACCCCTGCTCGTGTTACAGGCGGGGTTTTTCTTGTTGA
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SEQIDNO_6_1992_3584     CAAGAATCCTCACAATACCGCAGAGTCTAG-ACTCGTGGTGGACTTCTCTCAATTT---T
M62321                  CCGGCCTCATCCACCTCCACCAGAACATTGTGGACGTGCAGTACTTGTACGGGGTGGGGT
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SEQIDNO_6_1992_3584     CTAGGGGGATCTCCCGTGTGTCTTGGCCAAAATTCGCAGTCCCCAACCTCCAATCACTCA
M62321                  CAAGCATCGCGTCCTGGGCCATTAAGTGGGAGTACGTCGTTCTCCTGTTCCTTCTGCTTG
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SEQIDNO_6_1992_3584     CCAACCTCCTGTCCTCCAATTTGTCCTGGTTATCGCTGGATGTGTCT------GCGGCGT
M62321                  CAGACGCGCGCGTCTGCTCCTGCTTGTGGATGATGCTACTCATATCCCAAGCGGAGGCGG
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SEQIDNO_6_1992_3584     TTTATCATATTCCTCTTCATCCTGCTGC--TATGCCTCATCTTCTTATTGGTTCTTCTGG
M62321                  CTTTGGAGAACCTCGTAATACTTAATGCAGCATCCCTGGCCGGGACGCACGGTCTTGTAT
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SEQIDNO_6_1992_3584     GACCATGCAAAACCTG---CACGACTCCTGCTCAAGGCAACTCTATGTTTCCCTCATGTT
M62321                  GTCTACACCTTCTACGGGATGTGGCCTCTCCTCCTG-CTCCTGTTGGCGTTGCCCCAGCG
                        * * *  *       *      * *  ** ***  * *  ** * *  * *  * *  *

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M62321                  GGCGTACGCGCTGGACACGGAGGTGGCCGCGTCGTGTGGCGGTGTTGTTCTCGTCGGGTT
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SEQIDNO_6_1992_3584     G--GGCTTTCGCAAAATACCTATGGGAGTGGGCCTCAGTCCGTTTCT-CTTGGCTCAGTT
M62321                  GATGGCGCTGACTCTGTCACCATATTACAAGCGCTATATCAGCTGGTGCTTGTGGTGGCT
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M62321                  T--CAGTATTTTCTGACCAGAGTGGAAGCGCAACTGCACGTGTGGATTCCCCCCCTCAAC
                        *   ***    * **  *** *       *    * * *     * **  *    *** *

SEQIDNO_6_1992_3584     -TATATGGATGATGTGGTATTGGGGGCCAAGTC---TGTACAGCATCGTGAGTCCCTTTA
M62321                  GTCCGAGGGGGGCGCGACGCCGTCATCTTACTCATGTGTGCTGTACACCCGACTCTGGTA
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SEQIDNO_6_1992_3584     TACCGCTGTTACCAATTTTCTTTTGTC--TCTGGGTATACATT-----------------
M62321                  T-TTGACATCACCAAATTGCTGCTGGCCGTCTTCGGACCCCTTTGGATTCTTCAAGCCAG
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SEQIDNO_6_1992_3584     ------------------------------------------------------------
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clustalw.dnd

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(SEQIDNO_6_1992_3584:0.37351,M62321:0.37351);
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Select tree menu Exec

OIPE IAP18 NOV 0 2 2005 PATENT & TRADEMARK OFFICE

CLUSTALW Result

[clustalw.aln][clustalw.dnd][readme]

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 CLUSTAL W (1.83) Multiple Sequence Alignments


Sequence type explicitly set to DNA
Sequence format is Pearson
Sequence 1: SEQIDNO_6_1992_3584     1593 bp
Sequence 2: X02763                  3221 bp
Start of Pairwise alignments
Aligning...


Sequences (1:2) Aligned. Score: 19.209
Sequences (2:2) Aligned. Score: 39.4908
Guide tree        file created:   [clustalw.dnd]
Start of Multiple Alignment
There are 1 groups
Aligning...
Group 1:                      Delayed
Sequence:2     Score:21165
Alignment Score 6911
CLUSTAL-Alignment file created  [clustalw.aln]
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clustalw.aln

CLUSTAL W (1.83) multiple sequence alignment

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X02763                   AGACACCGCCTCAGCTCTGTATCGAGAAGCCTTAGAGTCTCCTGAGCATTGCTCACCTCA

SEQIDNO_6_1992_3584      ------------------------------------------------------------
X02763                   CCATACTGCACTCAGGCAAGCCATTCTCTGCTGGGGGGAATTGATGACTCTAGCTACCTG

SEQIDNO_6_1992_3584      ------------------------------------------------------------
X02763                   GGTGGGTAATAATTTGGAAGATCCAGCATCTAGGGATCTTGTAGTAAATTATGTTAATAC

SEQIDNO_6_1992_3584      ------------------------------------------------------------
X02763                   TAACGTGGGTTTAAAGATCAGGCAACTATTGTGGTTTCATATATCTTGCCTTACTTTTGG
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SEQIDNO_6_1992_3584     ------------------------------------------------------------
X02763                  AAGAGAGACTGTACTTGAATATTTGGTCTCTTTCGGAGTGTGGATTCGCACTCCTCCAGC

SEQIDNO_6_1992_3584     ------------------------------------------------------------
X02763                  CTATAGACCACCAAATGCCCCTATCTTATCAACACTTCCGGAAACTACTGTTGTTAGACG

SEQIDNO_6_1992_3584     ----------------------------ATGGATGCAATGAAGAGAGGGCTCTGCTGTGT
X02763                  ACGGGACCGAGGCAGGTCCCCTAGAAGAAGAACTCCCTCGCCTCGCAGACGCAGATCTCC
                                                  *    * *   *    * * * * * * *

SEQIDNO_6_1992_3584     GCTGCTGCTGTGTGGAGCAGTCTTCGTTTCG-----CCCAGCGCTAGCG------AAACC
X02763                  ATCGCCGCGTCGCAGAA-GATCTCAATCTCGGGAATCTCAATGTTAGTATTCCTTGGACT
                           ** **   *  **    ***   * ***     * **  * ***          **

SEQIDNO_6_1992_3584     CACGTCACCGGGGGAAGTGCCGGCCACACTGTGTCTGGATTTGTTAGCCTC---CTCGCA
X02763                  CATAAGGTGGGAAACTTTACGGGGCTTTATTCCTCTACAGTACCTATCTTTAATCCTGAA
                        **       **      * * ** *    *   ***  * *   ** * *    *  * *

SEQIDNO_6_1992_3584     C--CAGGCGCC----------AAGCAGAACGTCCAGCTGATCAACACCAACGGCAGTTGG
X02763                  TGGCAAACTCCTTCCTTTCCTAAGATTCATTTACAAGAGGACATTATTAATAGGTGTCAA
                           **  * **          ***    *  * **   *  **  *  **  *  **

SEQIDNO_6_1992_3584     CACCTCAATAGCACGGCC-CTG-AACTGCAATGATAGCCTCAACACCGGCTG-GTTGGCA
X02763                  CAATTTGTGGGCCCTCTCACTGTAAATGAAAAGAGAAGATTGAAATTAATTATGCCTGCT
                        **  *     ** *   * *** ** ** ** ** *   *  * *     *  *   **

SEQIDNO_6_1992_3584     GGGCTTT--TCTATCACCAC-AAGTTCAACTCTTCAGGC------------------TGT
X02763                  AGATTCTATCCTACCCACACTAAATATTTGCCCTTAGACAAAGGAATTAAACCTTATTAT
                         *  * *   *** *  *** ** *      * * ** *                  * *

SEQIDNO_6_1992_3584     CCTGAGAGGCTAGCCAGCTGCCGACCCCTTACCG------ATTTTGACCAGGGCTGGGGC
X02763                  CCAGATCAGGTAGTTAATCATTACTTCCAAACCAGACATTATTTACATACTCTTTGGAAG
                        ** **   * ***  *          **  ***       ****  *       ***

SEQIDNO_6_1992_3584     CCTATCAGT-TATGCCAACGGAAGCGGCCCCGACCAGCGCCCC-TACTGCTGG-CAC--T
X02763                  GCTGGTATTCTATATAAGCGGGA--AACCACACGTAGCGCATCATTTTGCGGGTCACCAT
                         **   * * ***   * *** *    ** *    *****  * *  *** ** ***  *

SEQIDNO_6_1992_3584     ACCCCCCAAAACC----TTGCGGTATTG-----TGCCCGCGAAGAGTGTGTGTGGTCC--
X02763                  ATTCTTGGGAACAAGAGCTACAGCATGGGAGGTTGGTCATCAAAACCTCGCAAAGGCATG
                        *  *     ***      * * * ** *     **  *   ** *    *    * *

SEQIDNO_6_1992_3584     --GGTATATTGCTTCACTCCCAGCCCCGTGGTGGTGGGAACGACCGACAGGTCGGGC---
X02763                  GGGACGAATCTTTCTGTTCCCAATCCTCTGGGATTCTTTCCCGATCATCAGTTGGACCCT
                          *    **   *    *****  **  ***   *     *     *   ** ** *

SEQIDNO_6_1992_3584     GCGCCCACCTACAGCTGGGGTGAAAATGATACGGACGTCTTCGTCCTTAACAATACCAGG
X02763                  GCATTCGGAGCCAACTCAAACAATCCAGATTGGGACTTCAACCCCGTCAAGGACGACTGG
                        **   *     ** **      *    ***  **** **  *  * * **  *   * **

SEQIDNO_6_1992_3584     CCACC-GCTGGGCAATT-GGTTCGGTTGTACCTGGATGAA--CTCAACTGGATTCACCAA
X02763                  CCAGCAGCCAACCAAGTAGGAGTGGGAGCATTCGGGCCAAGGCTCACCCCTCCACACGGC
                        *** * **    *** * **   **  * *   **   **  **** *      ***

SEQIDNO_6_1992_3584     AGTGTGC-GGAGCGCCTCCTTGTGTCATCGGAGGGGCGGGCAACAACACCCTGCACTGCC
X02763                  GGTATTTTGGGGTGGAGCCCTCAGGCTCAGGGCATATTGACCACAGTGTCAACAATTCCT
                         ** *   ** * *   ** *  * *   **       * * ***    *    * * *

SEQIDNO_6_1992_3584     CCAC-TGATTGCTTCCGCAAGCATCCGG--ACGCCACATACTCTCGGTGCGGCTCCGGTC
X02763                  CCTCCTGCCTCCACCAATCGGCAGTCAGGAAGGCAGCCTACTCCCATCTCTCCACCTCTA
                        ** * **  * *  *     ***  * *  * **  * ***** *    *  * **  *
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SEQIDNO_6_1992_3584     CCTGGATCACACCCAGGTGCCTGGTCGACTACCCGTATAGGCTTTGGCATTATCCTTGTA
X02763                  AGAGACAGTCATCCTCAGGCCATGCAGTGGAATTCCACTGCCTTCCAC-CAAACTCTGCA
                           *     ** **    ***  *  *   *     *  * ***   *   * *  ** *

SEQIDNO_6_1992_3584     CCATCAACTACACCATATTTAAAATCAGGATGTACGTGGGAGGGGTCGAACACAGGCTGG
X02763                  GGATCCCAGAGTCAGGGGTCTGTATCTTCCTGCTGGTGGCTCCAGTTCAGGA-ACAGTAA
                          ***    *  *     *    ***    **   ****     **  *  * *   *

SEQIDNO_6_1992_3584     AAGCTGCCTGCAAC-TGGACGCGGGGCGAACGTTGCGATCTG-GAAGATAGGGACAGGTC
X02763                  ACCCTGCTCCGAATATTGCCTCTCACATCTCGTCAATCTCCGCGAGGACTGGGG--ACCC
                        *  ****    **  * * * *        ***     ** * ** **  ***      *

SEQIDNO_6_1992_3584     CGAGATCGATATGGAGAACATCACATCAGGATTCCTAGGACCCCTGCTCGTGTTACAGGC
X02763                  TGTGACGAACATGGAGAACATCACATCAGGATTCCTAGGACCCCTGCTCGTGTTACAGGC
                         * **   * **************************************************

SEQIDNO_6_1992_3584     GGGGTTTTTCTTGTTGACAAGAATCCTCACAATACCGCAGAGTCTAGACTCGTGGTGGAC
X02763                  GGGGTTTTTCTTGTTGACAAGAATCCTCACAATACCGCAGAGTCTAGACTCGTGGTGGAC
                        ************************************************************

SEQIDNO_6_1992_3584     TTCTCTCAATTTTCTAGGGGGATCTCCCGTGTGTCTTGGCCAAAATTCGCAGTCCCCAAC
X02763                  TTCTCTCAATTTTCTAGGGGGATCTCCCGTGTGTCTTGGCCAAAATTCGCAGTCCCCAAC
                        ************************************************************

SEQIDNO_6_1992_3584     CTCCAATCACTCACCAACCTCCTGTCCTCCAATTTGTCCTGGTTATCGCTGGATGTGTCT
X02763                  CTCCAATCACTCACCAACCTCCTGTCCTCCAATTTGTCCTGGTTATCGCTGGATGTGTCT
                        ************************************************************

SEQIDNO_6_1992_3584     GCGGCGTTTTATCATATTCCTCTTCATCCTGCTGCTATGCCTCATCTTCTTATTGGTTCT
X02763                  GCGGCGTTTTATCATATTCCTCTTCATCCTGCTGCTATGCCTCATCTTCTTATTGGTTCT
                        ************************************************************

SEQIDNO_6_1992_3584     TCTGGATTATCAAGGTATGTTGCCCGTTTGTCCTCTAATTCCAGGATCAACAACAACCAG
X02763                  TCTGGATTATCAAGGTATGTTGCCCGTTTGTCCTCTAATTCCAGGATCAACAACAACCAG
                        ************************************************************

SEQIDNO_6_1992_3584     TACGGGACCATGCAAAACCTGCACGACTCCTGCTCAAGGCAACTCTATGTTTCCCTCATG
X02763                  TACGGGACCATGCAAAACCTGCACGACTCCTGCTCAAGGCAACTCTATGTTTCCCTCATG
                        ************************************************************

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X02763                  TTGCTGTACAAAACCTACGGATGGAAATTGCACCTGTATTCCCATCCCATCGTCCTGGGC
                        ************************************************************

SEQIDNO_6_1992_3584     TTTCGCAAAATACCTATGGGAGTGGGCCTCAGTCCGTTTCTCTTGGCTCAGTTTACTAGT
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                        ************************************************************

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X02763                  GCCATTTGTTCAGTGGTTCGTAGGGCTTTCCCCCACTGTTTGGCTTTCAGCTATATGGAT
                        ************************************************************

SEQIDNO_6_1992_3584     GATGTGGTATTGGGGGCCAAGTCTGTACAGCATCGTGAGTCCCTTTATACCGCTGTTACC
X02763                  GATGTGGTATTGGGGGCCAAGTCTGTACAGCATCGTGAGTCCCTTTATACCGCTGTTACC
                        ************************************************************

SEQIDNO_6_1992_3584     AATTTTCTTTTGTCTCTGGGTATACATT------------------------------
X02763                  AATTTTCTTTTGTCTCTGGGTATACATTTAAACCCTAACAAAACAAAAAGATGGGGTTAT
                        ****************************

SEQIDNO_6_1992_3584     ------------------------------------------------------------
X02763                  TCCCTAAACTTCATGGGCTACATAATTGGAAGTTGGGGAACTTTGCCACAGGATCATATT
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SEQIDNO_6_1992_3584     ------------------------------------------------------------
X02763                  CCTGCCTTAATGCCTTTGTATGCATGTATACAAGCTAAACAGGCTTTCACTTTCTCGCCA

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SEQIDNO_6_1992_3584     ------------------------------------------------------------
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X02763                  GCCGCTTGTTTTGCTCGCAGCCGGTCTGGAGCAAAGCTCATCGGAACTGACAATTCTGTC

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X02763                  ACTTCAAAGACTGTGTGTTTAAGGACTGGGAGGAGCTGGGGGAGGAGATTAGGTTAAAGG

SEQIDNO_6_1992_3584     ------------------------------------------------
X02763                  TCTTTGTATTAGGAGGCTGTAGGCACAAATTGGTCTGCGCACCAGCAC
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(SEQIDNO_6_1992_3584:0.40395,X02763:0.40395);
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